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A-378CIP5.ST25.txt
SEQUENCE LISTING

MAY 25 2001

TECH CENTER 1600/2900

<110> BOYLE, WILLIAM
LACEY, DAVID
CALZONE, FRANK
CHANG, MING-SHI
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

<130> A-378CIP5

<140> US 09/613,591

<141> 2000-07-10

<150> US 09/457,647

<151> 1999-12-09

<150> US 09/350,670

<151> 1999-07-09

<150> US 08/706,945

<151> 1996-09-03

<150> US 08/577,788

<151> 1995-12-22

<160> 168

<170> PatentIn version 3.0

<210> 1

<211> 36

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<213> Artificial

<220>

<223> Random cDNA with internal NotI restriction site.

<220>

<221> misc_feature

<222> (16, 17, 18, 19, 20, 21, 22 and)..(23)

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36

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<211> 16

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<213> Artificial

<220>

<223> ds oligonucleotide adapter

<400> 2

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16

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tgtaaacga cggccagt 18

<210> 5
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<220>
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<400> 5
caggaaacag ctatgacc 18

<210> 6
<211> 20
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<220>
<223> T3 primer

<400> 6
caattaacc tcactaaagg 20

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<211> 23
<212> DNA
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<400> 7
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<210> 8
<211> 23
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<213> Rattus rattus

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<211> 30
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<220>
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gactagtccc acaatgaaca agtggctgtg 30

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 ataagaatgc ggccgctaaa ctatgaaaca gccagtgac cattc 45

<210> 11
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 <212> DNA
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<220>
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<400> 11
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<210> 12
 <211> 21
 <212> DNA
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<220>
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<400> 12
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<210> 13
 <211> 24
 <212> DNA
 <213> Rattus rattus

<400> 13
 atcaaaggca gggcatactt cctg 24

<210> 14
 <211> 24
 <212> DNA
 <213> Rattus rattus

<400> 14
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<210> 15
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<400> 15
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<212> DNA
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 <210> 17
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 <210> 18
 <211> 31
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 <210> 19
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 <210> 22
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 <400> 23
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<210> 24
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 <212> DNA
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 <220>
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 <400> 27
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 <400> 30

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<210> 31
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<400> 31

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 1 5 10 15

Gln Leu Leu

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<400> 32

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<210> 33
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<400> 33

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<210> 34
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<400> 34

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<210> 35
 <211> 34
 <212> DNA
 <213> Mus musculus

<400> 35

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<400> 36

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<400> 37

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<210> 38
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<400> 38
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<210> 39
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<212> DNA
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<400> 39
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<210> 40
<211> 35
<212> DNA
<213> Mus musculus

<400> 40
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<210> 41
<211> 40
<212> DNA
<213> Mus musculus

<400> 41
cctctgtcga ctattataag cagcttattt tcacggattg 40

<210> 42
<211> 21
<212> DNA
<213> Mus musculus

<400> 42
tcccttgccc tgaccactct t 21

<210> 43
<211> 35
<212> DNA
<213> Mus musculus

<400> 43
cctctgtcga cttaacacac gttgtcatgt gttgc 35

<210> 44
<211> 21
<212> DNA
<213> Mus musculus

<400> 44
tcccttgccc tgaccactct t 21

<210> 45
<211> 35
<212> DNA

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<213> Mus musculus

<400> 45

cctctgtcga cttacttttg cgtggcttct ctgtt

35

<210> 46

<211> 1548

<212> DNA

<213> Artificial

<220>

<223> Human sequence modified to include unique AatII and SacII sites.

<400> 46

tgcacgcatt gcatacgtac cagaggggta cgctctcatc ccttgacggt ccgtagttta	60
ttttgctttc cgagtcagct ttctgacccg gaaagcaaaa tagacaacaa acagccactt	120
gcgagaggac tcctcctgtt taggcggccc tcgcctaaac ttgcaacgct tcgttgccgg	180
gcctcccacc gccgctcctg cgggcgggtat ttgacgggtcc gtagtttaaat tcgtcttccg	240
gtaggactgc ctaccggaaa aacgcaaaga tgtttgagaa aacaaataaa aagattttatg	300
taagtttata cctgcagcat gaattgaaaa ttctataccc gttagttaac gaggacaatt	360
ttaacgaaat ctttatgaaa ccgtcgccaa acaacataac tcaaagtaaa cgcgtaacca	420
atttaccttt cactggcacg cgaatgatgt cggattataa aaactttata gggttctcga	480
aaaaggaagc gtacgggtgc gatttgtaag aaaaagagaa aaccaattta gcaacaaact	540
aaataataaa cgatataaat aaaaagctat taatagttga tctcttcctt gttaattacc	600
atacaagtat gtgcgtacat ttttatttga tagatatatc aacagaaaga gacttacacg	660
ttttgattcg taaggcttcg gtaataatcg tcatacttat ccctttgatt tgggtcacta	720
ttctggacta ctaaagcgaa gaaattaatg taaacctcta aaaaataaat gtcgtaacaa	780
aagtttatat aagggttaatt agccacttac taacctcaat cttattagat gatatactag	840
tataaaataa tttaatcgca gtagtattat aacggaggta aaaaatccca ttaataggtc	900
ttaactttat agtctaaatt ggtatcttac tcctatttac tagcgctcat ttattataag	960
tgttacatgg taaaatcagt atagtctatt cgtaactaat tatagtaata acgaagatgt	1020
ccgaaattaa aataattaat aagacattca cagcagccgt aaatacagaa agtatgggta	1080
gagaaatagg aatggataac aaacagcggt caaacgcac aatataatag aattttgcc	1140
ttatctaact gtaaactaag attatttaac ctaaaaacag tgtgataata tagcgaactt	1200
tatgttaaca aattgtattc atggacatcc tagcatgtcc aatgcggtc ttttaccaaa	1260
caatatcagc taattagcta aactaagatc taaacaaaat tgattaattt cctccttatt	1320
gtataccaat tgcgcaacct taagctcgag tgatcacagc tggacgtccc atgggtacct	1380
cgaatgagct cctaggcgcc tttcttcttc ttcttcttct ttcgggcttt ccttcgactc	1440
aaccgacgac ggtggcgact cgttattgat cgtattgggg aaccccgag atttgcccag	1500
aactcccaa aaaacgactt tcctccttgg cgagaagtgc gagaagtg	1548

<210> 47
 <211> 48
 <212> DNA
 <213> Homo sapiens

<400> 47
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<210> 48
 <211> 55
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer

<400> 48
 cgatttgatt ctagaaggag gaataacata tgggtaacgc gttggaattc ggtac 55

<210> 49
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer

<400> 49
 taaactaaga tcttcctcct tattgtatac caattgcgca accttaagc 49

<210> 50
 <211> 1546
 <212> DNA
 <213> Artificial

<220>
 <223> Human sequence modified to include unique AatII and SacII sticky ends

<220>
 <221> misc_feature
 <222> (1, 2, 1545 and)..(1546)
 <223> Unique AatII and SacII sticky ends

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 cgaaaggctc agtcgaaaga ctgggccttt cgttttatct gttgtttgtc ggtgaacgct 120
 ctcttgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccgga 180
 ggggtggcggg caggacgcc gccataaact gccaggcatc aaattaagca gaaggccatc 240
 ctgacggatg gcctttttgc gtttctacaa actcttttgc ttatttttct aaatacatc 300
 aaatatggac gtcgtactta actttttaaag tatgggcaat caattgctcc tgttaaaatt 360
 gctttagaaa tactttggca gcgggttggt gtattgagtt tcatttgccg attgggttaa 420
 tggaaagtga ccgtgcgctt actacagcct aatatttttg aaatatccca agagcttttt 480
 ccttcgcatg cccacgctaa acattctttt tctcttttgg ttaaactcgtt gtttgattta 540

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ttcatacacg catgtaaaaa taaactatct atatagttgt ctttctctga atgtgcaaaa 660
ctaagcattc cgaagccatt attagcagta tgaataggga aactaaacc agtgataaga 720
cctgatgatt tcgcttcttt aattacattt ggagattttt tatttacagc attgttttca 780
aatatattcc aattaatcgg tgaatgattg gagttagaat aatctactat aggatcatat 840
tttattaaat tagcgtcatc ataatatgtc ctccattttt tagggtaatt atccagaatt 900
gaaatatcag atttaaccat agaatgagga taaatgatcg cgagtaaata atattcacia 960
tgtaccattt tagtcatatc agataagcat tgattaatat cattattgct tctacaggct 1020
ttaattttat taattattct gtaagtgtcg tcggcattta tgtctttcat acccatctct 1080
ttatccttac ctattgtttg tcgcaagttt tgcgtgttat atatcattaa aacggtaata 1140
gattgacatt tgattctaataaattggatt tttgtcacac tattatatcg cttgaaatac 1200
aattgtttta cataagtacc tgtaggatcg tacaggttta cgcaagaaaa tggtttggtta 1260
tagtcgatta atcgatttga ttctagattt gtttttaacta attaaaggag gaataacata 1320
tggttaacgc gttggaattc gagctcacta gtgtcgacct gcagggtacc atggaagctt 1380
actcgaggat ccgcggaaaag aagaagaaga agaagaaaag ccgaaaggaa gctgagttgg 1440
ctgctgccac cgctgagcaa taactagcat aacccttgg ggctctaaa cgggtcttga 1500
gggggttttt gctgaaagga ggaaccgctc ttcacgctct tcacgc 1546

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<210> 51
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 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 51
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<210> 52
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 52
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<210> 53
 <211> 141
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 53

A-378CIP5.ST25.txt

ctaattccga tctcacctac caaacaatgc ccccttgcaa aaaataaatt catataaaaa 60
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tggcgggtgat actgagcaca t 141

<210> 54
<211> 147
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

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tttttgtatg tctattggta gacgccacta tttaatagag accgccacaa ctgtatttat 120
ggtgaccgcc actatgactc gtgtagc 147

<210> 55
<211> 55
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 55
cgatttgatt ctagaaggag gaataacata tggtaacgc gttggaattc ggtac 55

<210> 56
<211> 49
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 56
taaactaaga tcttctcct tattgtatac caattgcgca accttaagc 49

<210> 57
<211> 668
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 57
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ttttgctttc cgagtcagct ttctgaccgc gaaagcaaaa tagacaacaa acagccactt 120
gcgagaggac tcactctgtt tagggcgccc tcgcctaaac ttgcaacgct tcgttgccgg 180
gcctcccacc gcccgctctg cggggcggtat ttgacggtcc gtagtttaat tcgtcttccg 240
gtaggactgc ctaccggaaa aacgcaaaga tgtttgagaa aacaaataaa aagatttatg 300
taagtttata cctgcagagt attaaaaatt ttttaagtaa actgtttacg attttaagaa 360

A-378CIP5.ST25.txt

ctaattataa gagttaacac tcgcgagtg taaatagcta aactaagatc taaactcaat	420
tgattaatatt cctccttatt gtataccaat tgcgcaacct taagctcgag tgatcacagc	480
tggacgtccc atgggtacctt cgaatgagct cctaggcgcc tttcttcttc ttcttcttct	540
ttcgggcttt ccttcgactc aaccgacgac ggtggcgact cgttattgat cgtattgggg	600
aaccccgag atttgcccag aactccccaa aaaacgactt tcctccttgg cgagaagtgc	660
gagaagtg	668

<210> 58
 <211> 726
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

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ctcctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccggg	180
gggtggcggg caggacgccc gccataaact gccaggcatc aaattaagca gaaggggcct	240
cccaccgccc gtccctgcggg cgggtatttga cgggtccgtag ttttaattcgt cttcgccatc	300
ctgacggatg gcctttttgc gtttctacaa actcctttgt ttatttttct aaatacatte	360
aaatatggac gtctcataat ttttaaaaaa ttcatttgac aaatgctaaa attcttgatt	420
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attaaaggag gaataacata tgggttaacgc gttggaattc gagctcacta gtgtcgacct	540
gcagggtacc atggaagctt actcgaggat ccgcggaaag aagaagaaga agaagaaagc	600
ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa taactagcat aacccttgg	660
ggcctctaaa cgggtcttga ggggtttttt gctgaaagga ggaaccgctc ttcacgctct	720
tcacgc	726

<210> 59
 <211> 44
 <212> DNA
 <213> Homo sapiens

<400> 59	
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<210> 60
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 60	
gtcctcctgg tacctaccta aaacaac	27

<210> 61

<211> 54
 <212> DNA
 <213> Homo sapiens

<400> 61
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<210> 62
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 62
 Met Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro
 1 5 10 15

Gly Thr Tyr

<210> 63
 <211> 84
 <212> DNA
 <213> Artificial

<220>
 <223> Sequence used in vector formation using human sequence with E. co
 li codon

<400> 63
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 gtgtgataaa tgtccgccgg gtac 84

<210> 64
 <211> 78
 <212> DNA
 <213> Artificial

<220>
 <223> Sequence used in vector formation using human sequence with E. co
 li codon

<400> 64
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 ttggaggaaa agtttcca 78

<210> 65
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer

<400> 65
 tacgcactgg atccttataa gcagcttatt ttcacggatt gaac 44

<210> 66
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer

 <400> 66
 gtgctcctgg tacctaccta aaacagcact gcacagtg 38

 <210> 67
 <211> 84
 <212> DNA
 <213> Artificial

 <220>
 <223> Part of oligonucleotide duplex used in vector formation

 <400> 67
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 gtgtgataaa tgtgctccgg gtac 84

 <210> 68
 <211> 78
 <212> DNA
 <213> Artificial

 <220>
 <223> Part of oligonucleotide duplex used in vector formation

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 ttggaggcag agtttcca 78

 <210> 69
 <211> 54
 <212> DNA
 <213> Mus musculus

 <400> 69
 tatggacca gaaactgggc atcagctgct gtgtgataaa tgtgctccgg gtac 54

 <210> 70
 <211> 48
 <212> DNA
 <213> Mus musculus

 <400> 70
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 <210> 71
 <211> 87
 <212> DNA
 <213> Artificial

 <220>
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 <400> 71
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 gctgtgtgat aaatgtgctc cgggtac 87

 <210> 72

<211> 81
 <212> DNA
 <213> Artificial

 <220>
 <223> Part of oligonucleotide duplex used in vector formation

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 <212> DNA
 <213> Artificial

 <220>
 <223> PCR primer

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 tgcattacga t 71

 <210> 74
 <211> 43
 <212> DNA
 <213> Mus musculus

 <400> 74
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 <210> 75
 <211> 76
 <212> DNA
 <213> Mus musculus

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 tgaacctgat tcccta 76

 <210> 76
 <211> 47
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 <213> Mus musculus

 <400> 76
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 <210> 77
 <211> 43
 <212> DNA
 <213> Homo sapiens

 <400> 77
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 <210> 78
 <211> 40
 <212> DNA

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<213> Homo sapiens

<400> 78
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40

<210> 79
<211> 40
<212> DNA
<213> Mus musculus

<400> 79
gttctcctca tatggaaact ctgcctccaa aatacctgca
40

<210> 80
<211> 43
<212> DNA
<213> Mus musculus

<400> 80
tacgcactgg atccttatgt tgcatttcct ttctgaatta gca
43

<210> 81
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 81
ccggaaacag ataatgag
18

<210> 82
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 82
gatcctcatt atctgttt
18

<210> 83
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 83
ccggaaacag agaagccacg caaaagtaag
30

<210> 84
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

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<400> 84
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<210> 85
 <211> 12
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 85
 tatgttaatg ag 12

<210> 86
 <211> 14
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 86
 gatcctcatt aaca 14

<210> 87
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 87
 tatgttccgg aaacagttaa g 21

<210> 88
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 88
 gatccttaac tgtttccgga aca 23

<210> 89
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> Part of oligonucleotide duplex used in vector formation

<400> 89
 tatgttccgg aaacagtga tcaactcaaa aataag 36

<210> 90
 <211> 38
 <212> DNA
 <213> Artificial

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<220>
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<400> 90
gatccttatt tttgagttga ttcactgttt ccggaaca 38

<210> 91
<211> 100
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 91
ctagcgacga cgacgacaaa gaaactctgc ctccaaaata cctgcattac gatccgga 60
ctgggtcatca gctgctgtgt cataaatgtg ctccgggtac 100

<210> 92
<211> 92
<212> DNA
<213> Artificial

<220>
<223> Part of oligonucleotide duplex used in vector formation

<400> 92
ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt 60
ttggaggcag agtttctttg tcgtcgtcgt cg 92

<210> 93
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

<400> 93
acaaacacaa tcgatttgat actaga 26

<210> 94
<211> 50
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

<400> 94
tttgttttaa ctaattaaag gaggaataaa atatgagagg atcgcatcac 50

<210> 95
<211> 50
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

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<400> 95
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<210> 96
<211> 49
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

<400> 96
aacctcccac cagctgctgt gcgacaaatg cccgccgggt acccaaaca 49

<210> 97
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

<400> 97
tgtttgggta cccggcgggc atttgt 26

<210> 98
<211> 50
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

<400> 98
cgcacagcag ctggtgggag gtttcttcgt cgtagtgcag gtatttcggc 50

<210> 99
<211> 49
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

<400> 99
gggaaggttt cgtgatggtg atggtgatgc catcctctca tattttatt 49

<210> 100
<211> 50
<212> DNA
<213> Artificial

<220>
<223> Used to produce fusion protein with human OPG

<400> 100
cctcctttaa ttagttaaaa caaatctagt atcaaatcga ttgtgtttgt 50

<210> 101
<211> 59
<212> DNA
<213> Homo sapiens

A-378CIP5.ST25.txt

<400> 101
acaaacacaa tcgatttgat actagatttg ttttaactaa ttaaaggagg aataaaatg 59

<210> 102
<211> 48
<212> DNA
<213> Homo sapiens

<400> 102
ctaattaaag gaggaataaa atgaaagaaa cttttcctcc aaaatatc 48

<210> 103
<211> 31
<212> DNA
<213> Homo sapiens

<400> 103
tgtttgggta cccggcggac atttatcaca c 31

<210> 104
<211> 59
<212> DNA
<213> Homo sapiens

<400> 104
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<210> 105
<211> 54
<212> DNA
<213> Homo sapiens

<400> 105
ctaattaaag gaggaataaa atgaaaaaaa aagaaacttt tcctccaaaa tatc 54

<210> 106
<211> 31
<212> DNA
<213> Homo sapiens

<400> 106
tgtttgggta cccggcggac atttatcaca c 31

<210> 107
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> PCR primer for FchOPG fusion protein.

<400> 107
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<210> 108
<211> 44
<212> DNA
<213> Artificial

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<220>
<223> PCR primer for FchOPG fusion protein

<400> 108
cgtttcatt ttaccgggc tgagcgagag gctcttctgc gtgt 44

<210> 109
<211> 45
<212> DNA
<213> Artificial

<220>
<223> PCR primer for FcmuOPG fusion protein

<400> 109
cgctcagccc gggtaaaatg gaaacgttgc ctccaaaata cctgc 45

<210> 110
<211> 39
<212> DNA
<213> Artificial

<220>
<223> PCR primer for FcmuOPG fusion protein

<400> 110
ccattttacc cgggctgagc gagaggctct tctgcgtgt 39

<210> 111
<211> 36
<212> DNA
<213> Artificial

<220>
<223> PCR primer for muOPG-Fc fusion protein

<400> 111
gaaaataaga tgcttagctg cagctgaacc aaaatc 36

<210> 112
<211> 34
<212> DNA
<213> Artificial

<220>
<223> PCR primer for muOPG-Fc fusion protein

<400> 112
cagctgcagc taagcagctt attttcacgg attg 34

<210> 113
<211> 36
<212> DNA
<213> Artificial

<220>
<223> PCR primer for huOPG-Fc fusion protein

<400> 113
aaaaataagc tgcttagctg cagctgaacc aaaatc 36

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<210> 114
<211> 35
<212> DNA
<213> Artificial

<220>
<223> PCR primer for huOPG-Fc fusion protein

<400> 114
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<210> 115
<211> 102
<212> DNA
<213> Artificial

<220>
<223> PCR primer for huOPG-Fc fusion protein

<220>
<221> misc_feature
<223> Linker with XbaI and KpnI sites inserted into human sequence.

<400> 115
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aactagtcac cagctgctgt gtgataaatg tccgccgggt ac 102

<210> 116
<211> 94
<212> DNA
<213> Artificial

<220>
<223> Linker with XbaI and KpnI sites inserted into human sequence

<400> 116
ccggcggaca tttatcacac agcagctgat gactagtttc ttcatacataa tgaagatatt 60
ttggagcaaa agtttccata tgttattcct cctt 94

<210> 117
<211> 62
<212> DNA
<213> Artificial

<220>
<223> Linker with XbaI and SpeI sites inserted into human sequence

<400> 117
ctagaaggag gaataacata tggaaacttt tcctgctaaa tatcttcatt atgatgaaga 60
aa 62

<210> 118
<211> 62
<212> DNA
<213> Artificial

<220>
<223> Linker with XbaI and SpeI sites inserted into human sequence

<400> 118

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ctagtttctt catcataatg aagatattta gcaggaaaag tttccatatg ttattcctcc 60
tt 62

<210> 119
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<212> PRT
<213> Homo sapiens

<400> 119

Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met
1 5 10 15
Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg
20 25 30
Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
35 40 45
Asp Trp His
50

<210> 120
<211> 2432
<212> DNA
<213> Rattus rattus

<220>
<221> CDS
<222> (124)..(1326)

<400> 120
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ggcagcagag aagcacctag cactggccca gcggctgccg cctgaggttt ccagaggacc 120
aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc 168
Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile 15
att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 216
Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr 30
gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 264
Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly 45
acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc 312
Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val 60
cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa 360
Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu 75
tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag 408
Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln 95
gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc 456
Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg 110
tac ctg gag ctc gaa ttc tgc ttg aag cac cgg agc tgt ccc cca ggc 504
Tyr Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly

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115				120				125				
ttg ggt gtg ctg cag gct ggg acc cca gag cga aac acg gtt tgc aaa	552											
Leu Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys												
130	135	140										
aga tgt ccg gat ggg ttc ttc tca ggt gag acg tca tcg aaa gca ccc	600											
Arg Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro												
145	150	155										
tgt agg aaa cac acc aac tgc agc tca ctt ggc ctc ctg cta att cag	648											
Cys Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln												
160	165	170	175									
aaa gga aat gca aca cat gac aat gta tgt tcc gga aac aga gaa gca	696											
Lys Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala												
180	185	190										
act caa aat tgt gaa ata gat gtc acc ctg tgc gaa gag gca ttc ttc	744											
Thr Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe												
195	200	205										
agg ttt gct gtg cct acc aag att ata ccg aat tgg ctg agt gtt ctg	792											
Arg Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu												
210	215	220										
gtg gac agt ttg cct ggg acc aaa gtg aat gca gag agt gta gag agg	840											
Val Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg												
225	230	235										
ata aaa cgg aga cac agc tcg caa gag caa act ttc cag cta ctt aag	888											
Ile Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys												
240	245	250	255									
ctg tgg aag cat caa aac aga gac cag gaa atg gtg aag aag atc atc	936											
Leu Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile												
260	265	270										
caa gac att gac ctc tgt gaa agc agt gtg caa cgg cat atc ggc cac	984											
Gln Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His												
275	280	285										
gcg aac ctc acc aca gag cag ctc cgc atc ttg atg gag agc ttg cct	1032											
Ala Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro												
290	295	300										
ggg aag aag atc agc cca gac gag att gag aga acg aga aag acc tgc	1080											
Gly Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys												
305	310	315										
aaa ccc agc gag cag ctc ctg aag cta ctg agc ttg tgg agg atc aaa	1128											
Lys Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys												
320	325	330	335									
aat gga gac caa gac acc ttg aag ggc ctg atg tac gca ctc aag cac	1176											
Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His												
340	345	350										
ttg aaa gca tac cac ttt ccc aaa acc gtc acc cac agt ctg agg aag	1224											
Leu Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys												
355	360	365										
acc atc agg ttc ttg cac agc ttc acc atg tac cga ttg tat cag aaa	1272											
Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys												
370	375	380										
ctc ttt cta gaa atg ata ggg aat cag gtt caa tca gtg aag ata agc	1320											
Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser												

385

390

395

tgc tta tagttaggaa tggctactgg gctgtttctt caggatgggc caacactgat 1376
 Cys Leu
 400
 ggagcagatg gctgcttctc cggtctctga aatggcagtt gattcctttc tcatcagttg 1436
 gtgggaatga agatcctcca gccaacaca cacactgggg agtctgagtc aggagagtga 1496
 ggcaggctat ttgataattg tgcaaagctg ccagggtgtac acctagaaag tcaagcacc 1556
 tgagaaagag gatattttta taacctcaaa cataggccct ttccttcctc tccttatgga 1616
 tgagtactca gaaggcttct actatcttct gtgtcatccc tagatgaagg cctcttttat 1676
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 tgatagtcta tgacattctt tttctacaa ttcgtatcag gtgcacgagc cttatcccat 1856
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 ttgcagactt ggctagacaa gcaggggtag gttatggtag tttatttaac agactgccac 1976
 caggagtcca gtgtttcttg ttcctctgta gttgtaccta agctgactcc aagtacattt 2036
 agtatgaaaa ataatcaaca aattttattc cttctatcaa cattggctag ctttgtttca 2096
 gggcactaaa agaaactact atatggagaa agaattgata ttgcccccaa cgttcaacaa 2156
 cccaatagtt tatccagctg tcatgcctgg ttcagtgtct actgactatg cgccctctta 2216
 ttactgcatg cagtaattca actggaaata gtaataataa taatagaaat aaaatctaga 2276
 ctccattgga tctctctgaa tatgggaata tctaacttaa gaagctttga gatttcagtt 2336
 gtgttaaagg cttttattaa aaagctgatg ctcttctgta aaagttacta atatatctgt 2396
 aagactatta cagtattgct atttatatcc atccag 2432

<210> 121
 <211> 401
 <212> PRT
 <213> Rattus rattus

<400> 121

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
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Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
 50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
 85 90 95
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
 100 105 110
 Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
 115 120 125
 Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140
 Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160
 Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
 165 170 175
 Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
 180 185 190
 Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205
 Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
 210 215 220
 Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255
 Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
 260 265 270
 Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala
 275 280 285
 Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly
 290 295 300
 Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
 305 310 315 320
 Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
 340 345 350

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Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 122
<211> 1325
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (91)..(1293)

<220>
<221> misc_feature
<223> At position 11, R is a purine.

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gctgcctcct gaggtttccc gaggaccaca atg aac aag tgg ctg tgc tgc gca 114
Met Asn Lys Trp Leu Cys Cys Ala
1 5
ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt 162
Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu
10 15 20
ctt cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg 210
Leu Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu
25 30 35 40
tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg 258
Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val
45 50 55
agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac 306
Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp
60 65 70
agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag 354
Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys
75 80 85
gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg 402
Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val
90 95 100
tgt gag tgt gag gaa ggg cgt tac ctg gag atc gaa ttc tgc ttg aag 450
Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
105 110 115 120
cac cgg agc tgt ccc ccg ggc tcc ggc gtg gtg caa gct gga acc cca 498

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His	Arg	Ser	Cys	Pro 125	Pro	Gly	Ser	Gly	Val 130	Val	Gln	Ala	Gly	Thr 135	Pro	
gag	cga	aac	aca	ggt	tgc	aaa	aaa	tgt	cca	gat	ggg	ttc	ttc	tca	ggt	546
Glu	Arg	Asn	Thr	Val	Cys	Lys	Lys	Cys	Pro	Asp	Gly	Phe	150	Ser	Gly	
			140					145								
gag	act	tca	tcg	aaa	gca	ccc	tgt	ata	aaa	cac	acg	aac	tgc	agc	aca	594
Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Ile	Lys	His	Thr	Asn	Cys	Ser	Thr	
		155					160					165				
ttt	ggc	ctc	ctg	cta	att	cag	aaa	gga	aat	gca	aca	cat	gac	aac	tgt	642
Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Cys	
	170					175					180					
tgt	tcc	gga	aac	aga	gaa	gcc	acg	caa	aag	tgt	gga	ata	gat	gtc	acc	690
Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	
185					190				195						200	
ctg	tgt	gaa	gag	gcc	ttc	ttc	agg	ttt	gct	ggt	cct	acc	aag	att	ata	738
Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	
				205					210					215		
cca	aat	tgg	ctg	agt	gtt	ttg	gtg	gac	agt	ttg	cct	ggg	acc	aaa	gtg	786
Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	
			220					225					230			
aat	gcc	gag	agt	gta	gag	agg	ata	aaa	cgg	aga	cac	agc	tca	caa	gag	834
Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	
		235					240					245				
caa	acc	ttc	cag	ctg	ctg	aag	ctg	tgg	aaa	cat	caa	aac	aga	gac	cag	882
Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	
	250					255					260					
gaa	atg	gtg	aag	aag	atc	atc	caa	gac	att	gac	ctc	tgt	gaa	agc	agc	930
Glu	Met	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	
265					270				275						280	
gtg	cag	cgg	cat	ctc	ggc	cac	tcg	aac	ctc	acc	aca	gag	cag	ctt	ctt	978
Val	Gln	Arg	His	Leu	Gly	His	Ser	Asn	Leu	Thr	Thr	Glu	Gln	Leu	Leu	
				285					290					295		
gcc	ttg	atg	gag	agc	ctg	cct	ggg	aag	aag	atc	agc	cca	gaa	gag	att	1026
Ala	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Ile	Ser	Pro	Glu	Glu	Ile	
			300					305					310			
gag	aga	acg	aga	aag	acc	tgc	aaa	tcg	agc	gag	cag	ctc	ctg	aag	cta	1074
Glu	Arg	Thr	Arg	Lys	Thr	Cys	Lys	Ser	Ser	Glu	Gln	Leu	Leu	Lys	Leu	
		315					320					325				
ctc	agt	tta	tgg	agg	atc	aaa	aat	ggt	gac	caa	gac	acc	ttg	aag	ggc	1122
Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	
	330					335					340					
ctg	atg	tat	gcc	ctc	aag	cac	ttg	aaa	aca	tcc	cac	ttt	ccc	aaa	act	1170
Leu	Met	Tyr	Ala	Leu	Lys	His	Leu	Lys	Thr	Ser	His	Phe	Pro	Lys	Thr	
345					350				355						360	
gtc	acc	cac	agt	ctg	agg	aag	acc	atg	agg	ttc	ctg	cac	agc	ttc	aca	1218
Val	Thr	His	Ser	Leu	Arg	Lys	Thr	Met	Arg	Phe	Leu	His	Ser	Phe	Thr	
				365					370					375		
atg	tac	aga	ctg	tat	cag	aag	ctc	ttt	tta	gaa	atg	ata	ggg	aat	cag	1266
Met	Tyr	Arg	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	
			380					385					390			
gtt	caa	tcc	gtg	aaa	ata	agc	tgc	tta	taactagga	tggtcactgg						1313

Val Gln Ser Val Lys Ile Ser Cys Leu
 395 400

gctgtttctt ca

1325

<210> 123
 <211> 401
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <223> At position 11, R is a purine.

<400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile
 1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp
 20 25 30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
 50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys
 165 170 175

Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205

A-378CIP5.ST25.txt

```

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
 210                               215                220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225                               230                235                240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
                245                               250                255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
                260                               265                270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser
                275                               280                285

Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly
 290                               295                300

Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
305                               310                315                320

Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
                325                               330                335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
                340                               345                350

Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
                355                               360                365

Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
 370                               375                380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385                               390                395                400

```

Leu

```

<210> 124
<211> 1356
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (95)..(1297)

```

```

<220>
<221> misc_feature
<223> At position 63, Y is a pyrimidine.

```

<400> 124

A-378CIP5.ST25.txt

gtatatataa	cgtgatgagc	gtacgggtgc	ggagacgcac	cggcgcgctc	gcccagccgc	60
cgycaccaag	cccctgaggt	ttccggggac	caca	atg aac aag ttg ctg tgc tgc	115	
				Met Asn Lys Leu Leu Cys Cys		
				1 5		
gcg ctc gtg ttt ctg gac atc tcc att aag tgg acc acc cag gaa acg	163					
Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr						
	10 15 20					
ttt cct cca aag tac ctt cat tat gac gaa gaa acc tct cat cag ctg	211					
Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu						
	25 30 35					
ttg tgt gac aaa tgt cct cct ggt acc tac cta aaa caa cac tgt aca	259					
Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr						
	40 45 50 55					
gca aag tgg aag tcc gtg tgc gcc cct tgc cct gac cac tac tac aca	307					
Ala Lys Trp Lys Ser Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr						
	60 65 70					
gac agc tgg cac acc agt gac gag tgt cta tac tgc agc ccc gtg tgc	355					
Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys						
	75 80 85					
aag gag ctg cag tac gtc aag cag gag tgc aat cgc acc cac aac cgc	403					
Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg						
	90 95 100					
gtg tgc gaa tgc aag gaa ggg cgc tac ctt gag ata gag ttc tgc ttg	451					
Val Cys Glu Cys Lys Glu Glu Arg Tyr Leu Glu Ile Glu Phe Cys Leu						
	105 110 115					
aaa cat agg agc tgc cct cct gga ttt gga gtg gtg caa gct gga acc	499					
Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr						
	120 125 130 135					
cca gag cga aat aca gtt tgc aaa aga tgt cca gat ggg ttc ttc tca	547					
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser						
	140 145 150					
aat gag acg tca tct aaa gca ccc tgt aga aaa cac aca aat tgc agt	595					
Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser						
	155 160 165					
gtc ttt ggt ctc ctg cta act cag aaa gga aat gca aca cac gac aac	643					
Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn						
	170 175 180					
ata tgt tcc gga aac agt gaa tca act caa aaa tgt gga ata gat gtt	691					
Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val						
	185 190 195					
acc ctg tgt gag gag gca ttc ttc agg ttt gct gtt cct aca aag ttt	739					
Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe						
	200 205 210 215					
acg cct aac tgg ctt agt gtc ttg gta gac aat ttg cct ggc acc aaa	787					
Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys						
	220 225 230					
gta aac gca gag agt gta gag agg ata aaa cgg caa cac agc tca caa	835					
Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln						
	235 240 245					
gaa cag act ttc cag ctg ctg aag tta tgg aaa cat caa aac aaa gcc	883					
Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Ala						

A-378CIP5.ST25.txt

250	255	260	
caa gat ata gtc aag aag atc atc caa gat att gac ctc tgt gaa aac Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn 265 270 275			931
agc gtg cag cgg cac att gga cat gct aac ctc acc ttc gag cag ctt Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu 280 285 290 295			979
cgt agc ttg atg gaa agc tta ccg gga aag aaa gtg gga gca gaa gac Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp 300 305 310			1027
att gaa aaa aca ata aag gca tgc aaa ccc agt gac cag atc ctg aag Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys 315 320 325			1075
ctg ctc agt ttg tgg cga ata aaa aat ggc gac caa gac acc ttg aag Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys 330 335 340			1123
ggc cta atg cac gca cta aag cac tca aag acg tac cac ttt ccc aaa Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys 345 350 355			1171
act gtc act cag agt cta aag aag acc atc agg ttc ctt cac agc ttc Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe 360 365 370 375			1219
aca atg tac aaa ttg tat cag aag tta ttt tta gaa atg ata ggt aac Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn 380 385 390			1267
cag gtc caa tca gta aaa ata agc tgc tta taactggaaa tggccattga Gln Val Gln Ser Val Lys Ile Ser Cys Leu 395 400			1317
gctgtttcct cacaattggc gagatcccat ggatgataa			1356

<210> 125
 <211> 401
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> At position 63, Y is a pyrimidine.

<400> 125

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile 1 5 10 15
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp 20 25 30
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr 35 40 45
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Ser Val Cys Ala Pro 50 55 60

A-378CIP5.ST25.txt

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln
 260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 275 280 285

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 290 295 300

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
 305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335

A-378CIP5.ST25.txt

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 126
<211> 139
<212> PRT
<213> Homo sapiens

<400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys
1 5 10 15

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
20 25 30

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala
35 40 45

Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys
50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr
65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn
85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His
100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly
115 120 125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys
130 135

<210> 127
<211> 48
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide capable of hybridizing to human sequence

<400> 127
acctacttct ttgaagagta gtcgacgaca cactattttac aggcggcc

48

<210> 128
<211> 219

<212> PRT

<213> Rattus rattus

<400> 128

```

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1      5      10      15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
      20      25      30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
      35      40      45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
      50      55      60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
      65      70      75      80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
      85      90      95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
      100      105      110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
      115      120      125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
      130      135      140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
      145      150      155      160
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
      165      170      175
Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
      180      185      190
Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
      195      200      205
Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
      210      215

```

<210> 129

<211> 281

<212> PRT

<213> Rattus rattus

<400> 129

```

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
1      5      10      15
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
      20      25      30
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
      35      40      45
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
      50      55      60
Gly Thr Tyr Leu Thr Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr
      65      70      75      80

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A-378CIP5.ST25.txt

Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
85 90 95

Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln
100 105 110

Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys
115 120 125

Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys
130 135 140

Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln
145 150 155 160

Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg
165 170 175

Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys
180 185 190

Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp
195 200 205

Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys
210 215 220

Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Thr Arg Thr Gln Arg Trp
225 230 235 240

Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
245 250 255

Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro
260 265 270

Ser Phe Ser Pro Thr Pro Gly Phe Thr
275 280

<210> 130
<211> 207
<212> PRT
<213> Rattus rattus

<400> 130

Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly
1 5 10 15

Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp
20 25 30

Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr
35 40 45

Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys
50 55 60

Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val
65 70 75 80

Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys
85 90 95

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys
100 105 110

A-378CIP5.ST25.txt

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys
 115 120 125
 Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr
 130 135 140
 Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro
 145 150 155 160
 Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn
 165 170 175
 Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Thr Ala Gly His Asn
 180 185 190
 Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr
 195 200 205
 <210> 131
 <211> 227
 <212> PRT
 <213> Rattus rattus
 <400> 131
 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Thr Thr Asp Gln
 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr

225

<210> 132
 <211> 197
 <212> PRT
 <213> Rattus rattus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr
 1 5 10 15
 Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu
 20 25 30
 His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
 35 40 45
 Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
 50 55 60
 Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80
 Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
 85 90 95
 Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
 100 105 110
 Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125
 Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
 130 135 140
 Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
 145 150 155 160
 Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln
 165 170 175
 Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met
 180 185 190
 Arg Ala Leu Leu Val
 195

<210> 133
 <211> 208
 <212> PRT
 <213> Rattus rattus

<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
 1 5 10 15
 Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 20 25 30
 Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
 35 40 45
 Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
 50 55 60
 Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys

```

65              70              75              80
Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
      85              90              95
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
      100             105             110
Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
      115             120             125
Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
      130             135             140
Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
      145             150             155             160
Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
      165             170             175
Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
      180             185             190
Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
      195             200             205

<210> 134
<211> 224
<212> PRT
<213> Rattus rattus

<400> 134
Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
1      5      10
Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
20     25     30
Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
35     40     45
Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
50     55     60
Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
65     70     75     80
Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
85     90     95
Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
100    105    110
Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
115    120    125
Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
130    135    140
Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145    150    155    160
Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165    170    175
Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180    185    190

```

A-378CIP5.ST25.txt

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

<210> 135
<211> 205
<212> PRT
<213> Rattus rattus

<400> 135

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu
1 5 10 15

Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro
20 25 30

Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val
35 40 45

Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro
50 55 60

Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr
65 70 75 80

Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro
85 90 95

Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln
100 105 110

Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly
115 120 125

His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys
130 135 140

Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp
145 150 155 160

Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr
165 170 175

Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp
180 185 190

Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val
195 200 205

<210> 136
<211> 191
<212> PRT
<213> Rattus rattus

<400> 136

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
35 40 45

A-378CIP5.ST25.txt

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
50 55 60
Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
65 70 75 80
His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
85 90 95
Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
100 105 110
Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
115 120 125
Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
130 135 140
Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
145 150 155 160
Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
165 170 175
Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu
180 185 190

<210> 137
<211> 54
<212> DNA
<213> Artificial

<220>
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54

<210> 138
<211> 284
<212> PRT
<213> Mus musculus

<400> 138

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala
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Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe
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Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn
35 40 45
Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His
50 55 60
Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile
65 70 75 80
Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
85 90 95
Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly
100 105 110

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Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser
 115 120 125
 Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
 130 135 140
 Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Ala Leu Cys
 145 150 155 160
 Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu
 165 170 175
 Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro
 180 185 190
 Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu
 195 200 205
 Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
 210 215 220
 Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe
 225 230 235 240
 Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His
 245 250 255
 Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
 260 265 270
 Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 275 280

<210> 139
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 139

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His
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 Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
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 Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr
 35 40 45
 Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro
 50 55 60
 Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His
 65 70 75 80
 Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe
 85 90 95
 Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala
 100 105 110
 Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe
 115 120 125
 Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His

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145                150                155                160
Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile
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                180                185                190
Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly
                195                200                205
Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser
                210                215                220
Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
225                230                235                240
Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys
                245                250                255
Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu
                260                265                270
Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala
                275                280                285
Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile
                290                295                300
Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
305                310                315                320
Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Lys His Phe
                325                330                335
Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His
                340                345                350
Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
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<220>
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 <210> 143
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 <210> 144
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 <220>
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<210> 159
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<212> DNA

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<210> 167

<211> 38

<212> DNA

<213> Artificial

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<223> PCR primer for deletion mutant

<400> 167

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38

<210> 168

<211> 16

<212> PRT

<213> Artificial

<220>

<223> Encoded by oligonucleotide duplex used in vector formation

<400> 168

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